

Original Research Article

<https://doi.org/10.20546/ijcmas.2020.903.211>

AMMI Biplot analysis for Stability of Grain Yield and Yield Contributing Traits in Promising Bio-Fortified Red Kernel Genotypes of Rice (*Oryza sativa* L.)

B. D. Waghmode^{1*}, M. R. Chavan², N. G. Sonone¹ and S. G. Bhav²

¹Agricultural Research Station, Shirgaon, Ratnagiri - 415 629 (MS), India

²Department of Agricultural Botany, Collage of Agriculture, Dapoli-415 712(MS), India

*Corresponding author

ABSTRACT

Genotype-environment interaction and stability performance were investigated on twenty genotypes of bio-fortified red kernel rice in three environments, at the experimental farm of Agricultural Research Station, Shirgaon, Agricultural Research Station, Phondaghat and department of Agricultural Botany farm, Dapoli (M.S.) during *Kharif* 2016. In interaction principle axis of AMMI biplot, first interaction principle axis (IPCA I) are favorable for all characters but second interaction principle axis (IPCA II) are favorable for eight characters. In AMMI 1 biplot, Dapoli location (E₃) favorable six for characters, Phondaghat location (E₂) favorable for three characters and Shirgaon location (E₁) favorable for eight traits. Both AMMI 1 and AMMI 2 biplot analysis was performed for grain yield plot⁻¹ since mean square for the IPCA I and IPCA II were found to be significant. AMMI 1 Biplot revealed that, genotypes, Bela and RTN-1211-6-1-4-1-11(6) fell almost on the horizontal line indicating uniform grain yield plot⁻¹ across the three environments. In AMMI 2 biplot Dapoli had short spokes and they did not exert strong interactive force while environments, Phondaghat and Shirgaon having long spokes exert strong interaction. Genotypes viz., RTN-1201-51-2-1-5-48, RTN-1211-5-1-3-5 and RTN-1201-5-1-3-14 were stable for Shirgaon and Dapoli environments for the traits viz., grain yield plant⁻¹, grain yield plot⁻¹, protein content (%), zinc content (ppm), iron content (ppm), amylose content (%), genotypes viz., RTN-1201-51-2-1-5-48 and RTN-1211-6-1-3-1-8 were stable for Shirgaon environment only, while as genotype RTN-1201-13-2-2-1-32 was stable for for all yield contributing characters across the three environments. The stable Genotype, RTN-1201-13-2-2-1-32 could be commercially exploited after testing in state multilocation and national trials or may be utilized for further studies

Keywords

Environments,
stable genotype,
IPCA,
Environments,
GxE interaction

Article Info

Accepted:
15 February 2020
Available Online:
10 March 2020

Introduction

Rice is the other name of food for Asian countries. It is an important source of carbohydrates, energy and protein in human diet. In the traditional growing areas of Asia,

rice varieties of various colors like red, purple, black, brown, yellow, and green have been cultivated and consumed. The coloured rice was preferred in earlier days due to taste and medicinal value. However, due to plant introduction and commercialization of

agriculture, colored rices are remaining unrecognized. Red rice is one of the prominent victims of this partiality. Red rices have a red bran layer. The color of the bran ranges from light to dark red. The bran layer contains polyphenols and anthocyanin, and possesses antioxidant properties. The red rices are a richer source of protein, zinc and iron than white rice.

The red landraces like Ptb 18, Ptb 19, Ptb 21, and Ptb 33, with broad-spectrum resistance to the brown plant hopper, have been used in resistance breeding programs all over the world. The nivararices have been used as sources of resistance to insect pests and viral diseases; Lalnakanda has been used as a drought resistance donor. Ptb 10 has been used for high photosynthetic activity. However, the true potential of red rice remained untapped due to the introduction of high yielding varieties and consumer preference for white rice.

The AMMI model (Gauch 1993) is more efficient in determining the most stable and high yielding genotypes in multi-environment trials compared to earlier procedures (Finlay and Wilkinson 1963, Eberhart and Russel 1966). Biplot analysis is possibly the most powerful interpretive tool for AMMI models. Biplots are graphs where aspects of both genotypes and environments are plotted on the same axes so that interrelationships can be visualized. The AMMI biplot where the main effects (genotype mean and environment mean) in X axis and IPCA1 scores for both genotypes and environments are plotted in Y axis. The effectiveness of AMMI procedure has been clearly demonstrated (Crossa *et al.*, 1991, Das *et al.*, 2009, Tarakanovas and Ruzgas 2006).

The multiplicative interaction model was first introduced by Crossa (1991), then adapted to the agricultural framework as AMMI by

Gauch and Zobel (1996). The main additive effect and multiplicative interaction (AMMI) analysis is a model that combines both additive and multiplicative components of a two way data structure that allows a breeder to obtain precise prediction on potential genotype and environmental effects on it (Akter *et al.*, 2014). This method has proven effective because it intercepts a large part of the GEI sum of square; it obviously separates main and interaction AMMI effects. The analysis not only serves an estimate of the total G x E interaction effect of each genotype but further partitions it into the environmental effects due to the interaction of the individual (Ebdon and Gauch, 2001). It combines the analysis for the genotypic and main environmental effect with several graphically represented interactions for principal component analysis (IPCA). Thus, it helps to summarize the pattern and relationship of genotypes, the environment, and their interaction. The aim of this research was to establish yield stability parameters in twenty bio-fortified red kernel lines to select the most valuable ones for the development of a stable variety.

Materials and Methods

The experiments were conducted at the experimental farm of Agricultural Research Station, Shirgaon (E₁), Agricultural Research Station, Phondaghat (E₂) and department of Agricultural Botany farm, Dapoli (E₃) during *Kharif* 2016. Twenty genotypes consisting of eighteen advanced lines *viz.*, RTN-1201-13-2-2-1-32 (1), RTN-1201-23-2-2-1-43 (2), RTN-1201-51-2-1-5-48 (3), RTN-1209-10-1-2-1-9 (4), RTN-1211-6-1-3-1-8 (5), RTN-1211-6-1-4-1-11 (6), RTN-1211-6-1-4-3-13 (7), RTN-1211-6-1-5-1-14 (8), RTN-1211-15-1-4-2-23 (9), RTN-1212-4-1-2-4 (10), RTN-1211-4-2-2-2 (11), RTN-1210-3-1-4-5 (12), RTN-1211-5-1-3-5 (13), RTN-1211-6-1-2-7 (14), RTN-1212-4-3-5-5 (15), RTN-1201-5-1-3-14

(16), RTN-1211-4-2-1-1 (17), RTN-1211-9-1-2-12 (18), and two red kernel pure line local check varieties, Bela,(19) and Patni-6 (20) were used. The experiments were carried using the randomized block design (RBD),with three replications. Twenty one days old seedlings were transplanted in plot size was 3m x 2m along with 20 cm x 15 cm spacing and two seedlings hill⁻¹. Line to line distance was 20 cm and plant to plant was 15 cm. There were 10 lines per plot and 20 hills per line with total 200 hills in each plot were transplanted. Standard agronomic practices were followed and plant protection measures were taken as required. Two border rows were maintained to minimize the border effects. Observations were recorded on average of 5 plant basis for 17 yield, yield contributing and quality traits *viz.*, days to 50 per cent flowering, plant height (cm), number of tillers plant⁻¹, number of panicles square meter⁻¹, panicle length plant⁻¹ (cm),total number of spikelets panicle⁻¹, number of filled spikelets panicle⁻¹, spikelet fertility (%), grain yield plant⁻¹ (g), straw yield plant⁻¹, grain yield plot⁻¹ (kg), straw yield plot⁻¹(kg), test weight (g), amylose content (%), protein content (%), zinc content (ppm) and iron content (ppm).Data were collected followed by standard method as described by Yoshida *et al.*, (1976).

Results and Discussion

AMMI analysis of variance

Numerous methods have been used for an understanding of the causes of G × E interaction. Among the multivariate approaches AMMI model is widely used (Gauch, 1988). The AMMI model describes the GE interaction in more than one dimension and it offers better opportunities for studying and interpreting GE interaction than analysis of variance (ANOVA) and regression of the mean (Zobel *et al.*, 1992). In

AMMI, the additive, portion is separated from interaction by ANOVA. Then the Interaction Principle Components Analysis (IIPCA), which provides a multiplicative model, is applied to analyze the interaction effect from the additive ANOVA model.

The AMMI analysis of variance for grain yield (kg/ha) plant⁻¹illustrated that 13.8245 of the total sum of square was attributable to environmental effects, only 1.8107 to genotypic effect, and 1.3485 to GEI effects (Table 1). The IPCA I captured 2.1734 of the interaction sum of square. Similarly, the IPCA II explained a further 0.4320 of the GEI sum of square and together with IPCA I and IPCA II contributed 2.6054 of the total GEI. Both AMMI 1 and AMMI 2 biplot analysis was performed for grain yield plot⁻¹ since mean square for the IPCA I and IPCA II were found to be significant.

Stability analysis by AMMI model

The GXE interaction was analyzed by AMMI model (Gauch 1988). The genotypes showed more interaction in characters *viz.*, Days to 50 per cent flowering, panicle length plant⁻¹, test weight (g), number of panicle square meter⁻¹, plant height (cm), amylose content (%), zinc content (ppm), and protein content (%). Environments showed more interaction in characters *viz.*, number of tillers plant⁻¹, spikelet fertility (%), grain yield plot⁻¹ (kg), total number of spikelets panicle⁻¹, number of filled spikelets panicle⁻¹, grain yield plant⁻¹ (g), straw yield plant⁻¹ (g), and iron content (ppm).

In AMMI 1 biplot, Dapoli location favorable for characters *viz.*, day to 50 per cent flowering, number of panicles square meter⁻¹, grain yield plant⁻¹, total number of spikelets panicle⁻¹, and number of filled spikelets panicle⁻¹. Phondaghat location favorable for characters *viz.*, spikelets fertility, amylose

content, protein content and Shirgaon location favorable for number of tillers plant⁻¹, panicle length, test weight, grain yield plot⁻¹, straw yield plot⁻¹ and plant⁻¹, plant height, iron and zinc content (Fig. 1).

Biplot analysis is possibly the most powerful interpretive tool for AMMI models. There are two basic AMMI biplots, the AMMI 1 biplot where the main effects (genotype mean and environment mean) and IPCA1 scores for both genotypes and environments are plotted against each other. On the other hand, the second biplot is AMMI 2 biplot where scores for IPCA1 and IPCA2 are plotted (Table 1). The mean grain yield value of genotypes averaged over environments indicated that the genotypes, RTN1211-6-1-2-7(14) and RTN1211-9-1-2-12(18) had the highest (6.09 tha⁻¹) and the lowest (5.0 tha⁻¹) yield, respectively. Different genotypes showed inconsistent performance across all environments. The environments mean grain yield ranged from 4.35 tha⁻¹ for E₁ to 7.21tha⁻¹ for E₂ and averaged grain yield over environments and genotypes is 5.57 tha⁻¹. On the basis of environmental index value in terms of negative and positive, E₁ and E₂ were poor, and E₃ was rich environment. Genotype, RTN-1211-4-2-1-1(17) is stable for grain yield plot⁻¹, grain yield plant⁻¹ and protein content. Genotype, RTN-1201-13-2-2-1-32(1) is most favorable for all the characters in the entire three environments; they give high yield, more content of micronutrients.

Stability analysis (AMMI model, Gauch 1988) identified the following genotypes as stable: RTN-1201-5-1-3-14(8) for day to 50 per cent flowering, RTN-1201-51-2-1-5-48(3) for plant height, RTN-1209-10-1-2-1-9(4) for panicle length, RTN-1211-4-2-1-1(17) for grain yields plot-1 and grain yield plant⁻¹, RTN-1201-23-2-2-1-43(2) for straw yield plot-1, Bela for straw yield plant⁻¹, RTN-1211-6-1-4-3-13(7) for zinc content, RTN-

1211-4-2-1-1(17) for protein content, RTN-1211-6-1-3-1-8(5) for iron content, RTN-1212-4-1-2-4(10) for amylose content and RTN-1211-6-1-4-1-11(6) for spikelets fertility, RTN-1211-5-1-3-5(13) for number of tillers plant⁻¹, RTN-1212-4-1-2-4(17) for test weight, RTN-1210-3-1-4-5(12) for number of panicles square meter⁻¹ and RTN-1211-5-1-3-5(13) for total number of spikelets panicle⁻¹. Nayak *et. al.* (2008), Vargas and Crossa (2000) Yan and Rajcan (2002), Bose *et. al.* (2014) and .Satoto *et. al.* (2016)

AMMI 1 biplot display

The AMMI 1 biplot gave a model fit 96.5%. This result is in agreement with the findings Gauch and Zobel (1996). Genotypes and environments on the same parallel line, relative or ordinate have similar yields and a genotype or environment on the right side of the midpoint of this axis has higher yields than those of left hand side.

Biplot are graphs where aspects of both genotypes and environments are plotted on the same axes so that inter relationships can be visualized. In the AMMI 1 biplot, the usual interpretation of biplot is that the displacements along the abscissa indicate differences in main (additive) effects, whereas displacements along the ordinate indicate differences in interaction effects. The best adapted genotype can plot far from the environment. If a genotype or an environment has IPCA1 score of nearly zero, it has small interaction effects and considered as stable. When a genotype and environment have the same sign on the PCA axis, their interaction is positive and if different, their interaction is negative. The AMMI 1 biplot expected yield clearly indicated for any genotype and environment combination can be calculated from Figure 1 following standard procedures suggested by Zobel *et al.*, (1988).

AMMI 1 biplot (Fig.1) analysis for grain yield plot⁻¹ depicted that the relative variability due to genotypes was less than the variability due environments as indicated by the distribution as well as position occupied by the twenty genotypes and three environments on biplot display (Fig. 15).

Genotypes or environments on right hand side of the vertical line showed higher grain yield plot⁻¹ than those on the left hand side. Thus, eight out of twenty genotypes namely, RTN-1201-13-2-2-1-32 (1), RTN-1201-23-2-2-1-43 (2), RTN-1201-51-2-1-5-48 (3), RTN-1211-6-1-4-3-13 (7), RTN-1211-4-2-2-2 (11), RTN-1210-3-1-4-5 (12), 15, RTN-1201-5-1-3-14 (16), and RTN-1211-4-2-1-1 (17) were identified to have higher grain yield plot⁻¹ with RTN-1211-6-1-4-3-13 (7) being the overall best with general mean of 4.43 kg. In contrast, the remaining of the genotypes were observed to show slightly low grain yield plot⁻¹ as they occupied the place farther from the left hand side of the main effect mid line on the biplot.

Among the test environments, two out of three environments namely, Phondaghat and Shirgaon seems to be most favourable environments as these occupied position on the right hand side of the midpoint of the main effect axis. The Dapoli environment was identified to be relatively unfavourable environment as they occupied position farther from the left hand side of the midpoint axis.

Perusal of Fig. 1 revealed that, genotypes, Bela and RTN-1211-6-1-4-1-11(6) fell almost on the horizontal line indicating uniform grain yield plot⁻¹ across the three environments.

However, it is to mention that three genotypes namely, RTN-1201-23-2-2-1-43(2), RTN-1211-4-2-1-1(17) and RTN-1211-4-2-2-2(11) were quite close to IPCA I axis and also plotted right hand side of the midpoint axis of main effect and therefore considered to be stable against the environmental changes with

minor positive and negative interactions. The genotypes, RTN-1201-13-2-2-1-32(1), RTN-1201-51-2-1-5-48(3), RTN-1211-4-2-1-1(17) and RTN-1212-4-3-5-5(15) fell on right hand side of the main effect axis but with large negative score on IPCA I and therefore, expected to perform better under Dapoli and Shirgaon environments.

Similarly, RTN-1201-23-2-2-1-43 (2), RTN-1211-6-1-4-3-13(7), RTN-1211-4-2-2-2(11), RTN-1210-3-1-4-5(12) and RTN-1201-5-1-3-14(8), had higher grain yield plot⁻¹ but positive score on IPCA I and therefore, expected to perform better on under Phondaghat and Shirgaon environments showing positive interaction with these environments. Kurniawan *et al.*, (2016), Bose *et. al.*(2014), Kulsum *et al.*, (2013).Nayaket. *al.* (2008), Vargas and Crossa (2000) Yan and Rajcan (2002), Bose *et. al.* (2014) and Satoto *et. al.* (2016)

AMMI 2 biplot display

The yield of grain plot⁻¹ showed slightly difference in each environment and these variation explained by AMMI analysis. They showed that the sum of square of environments is higher than the G X E interaction and genotypes, so major difference was due to environmental effect. These finding were in conformity to those of Temesgen *et al.*, (2015). The variance of GEI was partitioned among the first two interaction principle component axis (IPCA). Of which IPCA I exhibited 0.4069 sum of square of the total GEI, IPCA II was 0.2050 sum of square.

In AMMI 2 (Fig.2) biplot Dapoli (E₃) had short spokes and they did not exert strong interactive force while environments, Phondaghat (E₂) and Shirgaon(E₁) having long spokes exert strong interaction. Genotypes, RTN-1211-6-1-4-3-13(7), RTN-1211-9-1-2-12(18), RTN-1201-13-2-2-1-

32(1), RTN-1201-51-2-1-5-48(3), RTN-1211-6-1-4-1-11(6), RTN-1212-4-1-2-4(10) and RTN-1201-51-2-1-5-48(3) had high IPCA score and away from origin were most responsive. Genotypes, RTN-1211-6-1-3-1-8(5) and RTN-1201-13-2-2-1-32(1) were adapted to Phondaghat, genotypes, RTN-1212-4-1-2-4(10), RTN-1211-6-1-4-1-11(6) and RTN-1201-51-2-1-5-48(4) to Dapoli and RTN-1211-6-1-4-3-13(7) to be adapted to Shirgaon. Kurniawan *et al.*, (2016), Bose *et al.*, (2014) and Kulsum *et al.*, (2013), Nayak *et al.* (2008), Vargas and Crossa (2000) Yan and Rajcan (2002), Bose *et al.*, (2014) and Satoto *et al.*, (2016)

AMMI biplot analysis for micronutrients stability

The micronutrients viz. zinc, iron, protein and amylose content in red rice showed very low variation of mean at all three environments. The AMMI analysis of variance showed that G X E interaction environments sum of square was very less than that for genotypes, so major difference was due to genotypic effect on these four micronutrients.

The variance of GEI was partitioned among the first two interaction principle component axis (IPCA) of which IPCA I exhibited viz. zinc, iron, protein and amylose respectively 1.4023, 0.2182, 0.1015 and 0.4204 sum of square of the total GEI, IPCA II was viz. zinc, iron, protein and amylose respectively, 0.5661, 0.0545, 0.0596 and 0.2339 sum of square these implied that the interaction of the 20 rice genotypes with three environments. These finding were in conformity to those of Kurniawan *et al.*, (2016), Bose *et al.*, (2014) and Kulsum *et al.*, (2013).

AMMI 1 biplot relieved that interaction of environments was high and varied. Phondaghat and Shirgaon had positive interaction for iron, amylose and protein

while for zinc showed negative interaction. Dapoli had negative interaction for all micronutrients. The environment being on the right hand side of the midpoint of the main effect axis seemed to be favorable environment for micronutrients viz. zinc, iron, protein and amylose.

Genotypes, RTN-1211-9-1-2-12(12), RTN-1201-5-1-3-14(8), RTN-1211-4-2-2-2(11), RTN-1201-5-1-3-14(16), RTN-1211-6-1-5-1-14(8), RTN-1211-5-1-3-5(13), RTN-1211-6-1-4-3-13(7) and RTN-1201-23-2-2-1-43(2) had high mean and positive interaction were adapted to favorable environments. Genotype that grouped together that had similar adaptation while environments which grouped together influence the genotype in the same way Gauch and Zobel (1996).

Genotypes, RTN-1211-6-1-4-1-11(6) for iron, RTN-1211-4-2-2-2(11) and RTN-1212-4-1-2-4(10) for amylose, RTN-1211-6-1-4-3-13(7) for zinc, and RTN-1211-6-1-4-3-13(17) for protein showed score near to zero have had small interaction effect indicating that these varieties were less influenced by environments. All they found stable and recommended for all the three environments. Kurniawan *et al.*, (2016), Bose *et al.*, (2014) and Kulsum *et al.*, (2013). Bose *et al.*, (2014), Kulsum *et al.*, (2013). Nayak *et al.*, (2008), Vargas and Crossa (2000) Yan and Rajcan (2002), Bose *et al.*, (2014) and Satoto *et al.* (2016)

In AMMI 2biplot, for amylose, zinc and iron Dapoli environment and for protein, Phondaghat environment had short spokes and they did not exert strong interactive force while remaining all environments having long spokes exert strong interaction. Bose *et al.*, (2014), Kulsum *et al.*, (2013). Nayak *et al.*, (2008), Vargas and Crossa (2000) Yan and Rajcan (2002), Bose *et al.*, (2014) and Satoto *et al.*, (2016)

Table.1 Mean performance of genotypes over three environments for Different traits

GENOTYPES	DFB	PHT (cm)	NT (p⁻¹)	PT (/M⁻²)	PL (cm)	TS (Panicle⁻¹)	FS (%)	FP (%)	TW (g)
RTN-1201-13-2-2-1-32	112.00	113.73	7.62	122.00	24.33	180.89	160.00	86.87	20.08
RTN-1201-23-2-2-1-43	99.22	106.33	5.80	106.56	24.26	193.56	167.11	87.05	19.30
RTN-1201-51-2-1-5-48	88.56	110.05	6.49	103.89	25.97	162.33	141.22	88.45	24.81
RTN-1209-10-1-2-1-9	94.56	95.59	6.84	120.78	25.36	198.78	166.67	86.02	24.15
RTN-1211-6-1-3-1-8	102.11	101.49	5.57	111.44	25.46	190.00	163.67	88.52	22.16
RTN-1211-6-1-4-1-11	91.33	101.94	5.57	102.67	22.67	173.11	141.44	81.70	22.19
RTN-1211-6-1-4-3-13	95.89	106.44	6.27	110.11	25.62	162.22	140.56	86.33	22.06
RTN-1211-6-1-5-1-14	112.89	100.29	6.07	112.11	23.20	174.22	141.67	84.28	22.27
RTN-1211-15-1-4-2-23	102.56	88.47	6.08	101.44	22.16	168.22	125.33	82.11	23.34
RTN-1212-4-1-2-4	106.67	99.56	6.23	127.00	25.33	191.00	155.78	81.83	21.76
RTN-1211-4-2-2-2	95.00	96.70	6.13	116.89	23.69	170.56	136.11	78.04	19.43
RTN-1210-3-1-4-5	97.22	96.48	7.04	118.00	25.31	170.56	139.11	78.48	21.77
RTN-1211-5-1-3-5	98.11	97.20	6.71	127.22	22.09	172.00	143.11	83.48	21.35
RTN-1211-6-1-2-7	111.89	92.83	6.42	123.33	23.08	150.11	117.33	78.06	20.99
RTN-1212-4-3-5-5	119.67	98.96	5.90	124.89	24.40	154.33	124.56	85.65	21.48
RTN-1201-5-1-3-14	98.11	99.30	6.24	123.78	25.73	153.56	119.11	82.21	22.08
RTN-1211-4-2-1-1	87.44	97.59	6.09	117.89	24.03	223.22	170.89	77.57	18.84
RTN-1211-9-1-2-12	101.44	93.98	6.91	133.44	23.41	150.22	131.44	85.57	19.74
Ch-1 (Bela)	105.67	135.01	5.31	129.67	27.08	160.33	136.33	87.06	31.04
Ch-2 (Patni-6)	93.00	139.25	5.60	104.22	19.89	142.89	126.00	87.81	30.95
Mean	100.67	103.56	6.25	116.87	24.15	172.11	142.37	83.85	22.49

Table.1 Contd.: Mean performance of genotypes over three environments for Different traits

GENOTYPES	GY (g/ Plant ⁻¹)	SY(g/ Plant ⁻¹)	GY (kg/ Plot ⁻¹)	SY(kg/ Plot ⁻¹)	FC (PPM)	ZC (PPM)	PC(%)	AC(%)
RTN-1201-13-2-2-1-32	9.68	19.79	2.03	4.01	6.54	13.122	8.050	19.31
RTN-1201-23-2-2-1-43	8.43	20.58	2.11	3.93	6.09	16.322	7.778	21.23
RTN-1201-51-2-1-5-48	9.78	19.83	2.09	4.00	9.10	14.389	7.278	20.09
RTN-1209-10-1-2-1-9	9.20	18.17	1.98	3.47	6.71	14.922	5.967	18.44
RTN-1211-6-1-3-1-8	9.34	20.27	2.20	3.66	8.21	16.211	7.778	21.14
RTN-1211-6-1-4-1-11	8.26	19.18	2.08	3.66	8.64	15.333	6.167	20.78
RTN-1211-6-1-4-3-13	7.91	18.31	2.06	4.43	8.50	18.956	7.167	21.36
RTN-1211-6-1-5-1-14	9.17	18.60	2.08	3.56	7.16	16.878	7.611	24.18
RTN-1211-15-1-4-2-23	9.77	18.21	2.08	3.48	6.89	19.733	6.100	20.19
RTN-1212-4-1-2-4	9.01	18.56	2.20	3.73	5.40	17.278	7.300	19.39
RTN-1211-4-2-2-2	8.08	19.61	2.05	3.88	10.52	20.478	7.311	20.01
RTN-1210-3-1-4-5	8.79	21.25	2.30	3.96	10.23	19.011	7.444	23.00
RTN-1211-5-1-3-5	9.79	19.13	2.16	3.56	8.34	15.589	8.122	21.48
RTN-1211-6-1-2-7	9.14	19.20	2.34	3.40	9.83	15.189	6.611	15.81
RTN-1212-4-3-5-5	8.52	18.86	2.32	3.82	9.47	18.522	7.278	20.53
RTN-1201-5-1-3-14	9.91	19.56	2.12	4.08	9.91	17.756	7.456	22.23
RTN-1211-4-2-1-1	8.63	19.34	2.14	3.82	9.41	18.411	7.378	20.66
RTN-1211-9-1-2-12	7.49	19.81	1.92	3.56	10.01	28.167	7.011	18.54
Ch-1 (Bela)	8.51	19.86	2.23	3.64	10.81	15.356	8.422	18.59
Ch-2 (Patni-6)	7.31	21.08	2.22	3.68	9.92	17.167	8.533	16.98
Mean	8.84	19.46	2.14	3.77	8.59	17.439	7.338	20.20

Table.2 AMMI ANOVA of twenty genotypes of bio-fortified red kernel rice for eight different characters pooled over three environments

Sources	DF	MSS							
		Days to 50 per cent flowering	Plant height (cm)	Number of tillers plant ⁻¹	Number of panicles seq.meter ⁻¹	Panicle length	Total number of spikelets panicle ⁻¹	Number of filled spiklets panicle ⁻¹	Spikletfertility (%)
Trial	59	80.2825	161.3355	0.9316	99.9669	4.5440	1068.2733	865.4731	32.4021
Genotypes	19	246.8928*	500.3409*	0.9894*	287.0940*	7.5536*	1164.0221*	823.4865*	40.3687*
Environments	2	13.7388	0.0320	5.9769	12.6396	1.8547	7835.5103	5421.7485	161.8888
GxE Interaction	38	0.4796	0.3225	0.6372	10.9995	3.1807	664.2286	646.6625	21.6037
PCA I	20	0.7976	0.5605	0.6808	12.5624	4.5338	693.3206	677.0439	30.3390
IPCA II	18	0.1264	0.0581	0.5887	9.2629	1.6773	631.9041	612.9053	11.8977
Error	120	35.1944	16.6527	0.2860	13.2352	1.9059	217.5963	126.0370	11.3811
Total	179	50.0559	64.3415	0.4988	41.8227	2.7754	497.9870	369.7618	18.3098
*significant for 5%									

Source	DF	MSS								
		Test weight (g)	Grain yield plant ⁻¹ (g)	Straw yield plant ⁻¹ (g)	Grain yield plot ⁻¹ (kg)	Straw Yield plot ⁻¹	Iron content (ppm)	Zinc content (ppm)	Protein content (%)	Amylose content (%)
Trial	59	12.5594	1.9203	5.6701	0.4148	0.0907	2.8721	10.6581	0.5452	4.0399
Genotypes	19	32.5145*	1.8107*	2.3732*	0.1930*	0.0375*	7.8107*	30.2011*	1.528*	11.530*
Environments	2	27.8066	13.8245	62.6267	4.4888	0.1647	7.8545	8.3859	0.0082	3.3320
GxE Interaction	38	1.7793	1.3485	4.3208	0.3113	0.1134	0.1406	1.0062	0.0817	0.3320
PCA I	20	2.5208	2.1734	5.3027	0.4069	0.1564	0.2182	1.4023	0.1015	0.4204
PCA II	18	0.9554	0.4320	3.2298	0.2050	0.0656	0.0545	0.5661	0.0596	0.2339
Error	120	2.0103	0.3536	1.2168	0.0983	0.0302	0.3446	1.4909	0.0852	1.7039
Total	179	5.4873	0.8700	2.6847	0.2026	0.0502	1.1777	4.5125	0.2368	2.4738
*significant for 5%										

Table.3 Environmental means over three environments

GENOTYPES	Grain yield (t/ha ⁻¹)			
	Shirgaon (E 1)	Phondaghat (E2)	Dapoli (E 3)	Mean
RTN-1201-13-2-2-1-32 (RTNRRPL 1)	5.47	4.74	5.65	5.29
RTN-1201-23-2-2-1-43 (RTNRRPL 2)	5.29	5.42	5.78	5.49
RTN-1201-51-2-1-5-48(RTNRRPL 3)	6.33	5.60	4.38	5.44
RTN-1209-10-1-2-1-9(RTNRRPL 4)	4.35	6.07	5.08	5.16
RTN-1211-6-1-3-1-8(RTNRRPL 5)	5.31	4.90	6.95	5.73
RTN-1211-6-1-4-1-11(RTNRRPL 6)	5.47	6.04	4.74	5.42
RTN-1211-6-1-4-3-13(RTNRRPL 7)	4.51	6.12	5.42	5.36
RTN-1211-6-1-5-1-14(RTNRRPL 8)	5.55	5.29	5.42	5.42
RTN-1211-15-1-4-2-23(RTNRRPL 9)	5.03	5.70	5.55	5.42
RTN-1212-4-1-2-4(RTNRRPL 10)	5.29	4.82	7.08	5.73
RTN-1211-4-2-2-2(RTNRRPL 11)	5.47	5.18	5.34	5.34
RTN-1210-3-1-4-5(RTNRRPL 12)	7.21	6.35	4.45	5.99
RTN-1211-5-1-3-5(RTNRRPL 13)	6.77	4.95	5.18	5.63
RTN-1211-6-1-2-7(RTNRRPL 14)	6.85	5.49	5.96	6.09
RTN-1212-4-3-5-5(RTNRRPL 15)	6.17	5.26	6.69	6.04
RTN-1201-5-1-3-14(RTNRRPL 16)	5.65	5.00	5.94	5.52
RTN-1211-4-2-1-1(RTNRRPL 17)	5.42	4.97	6.33	5.57
RTN-1211-9-1-2-12(RTNRRPL 18)	4.43	5.16	5.42	5.00
Ch-1 (Bela) (RTNRRPL 19)	5.91	4.82	6.69	5.81
Ch-2 (Patni-6) (RTNRRPL 20)	4.43	4.82	8.07	5.78
Mean	5.55	5.34	5.81	5.57
CD at 5 %	0.43	0.34	0.66	
CV at 5 %	12.17	10.05	17.97	

Table.4 Genotypes are high yielding stable performance for three environments

Sr. No.	Genotypes	Favourable for character	Stable environments
1	RTN-1201-51-2-1-5-48, RTN-1211-5-1-3-5 and RTN-1201-5-1-3-14	grain yield plant ⁻¹ , grain yield plot ⁻¹ and micronutrients	Dapoli and Shirgaon
2	RTN-1201-13-2-2-1-32	For all yield contributing character	Dapoli, Shirgaon and Phondaghat
3	RTN-1201-51-2-1-5-48 and RTN-1211-6-1-3-1-8	Spikelet fertility, test weight, plant height, panicle length and micronutrients	Shirgaon

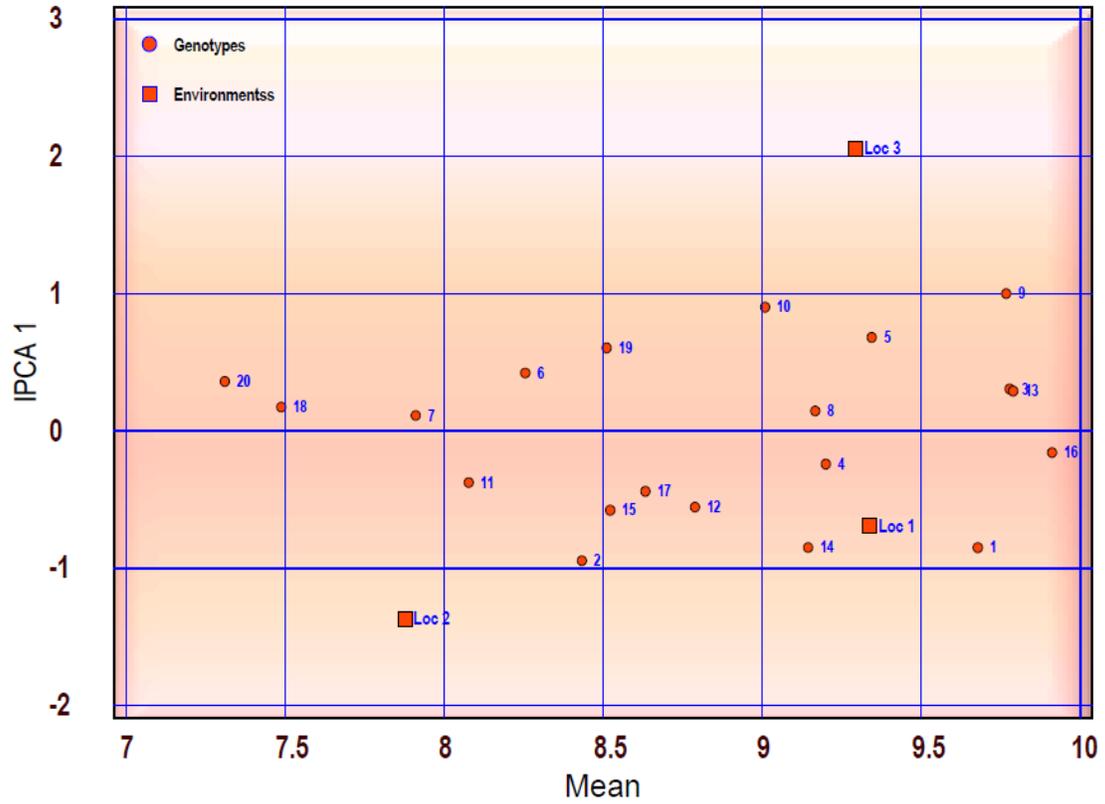


Fig.1 Biplot (AMMI 1) for grain yield plant⁻¹(g)

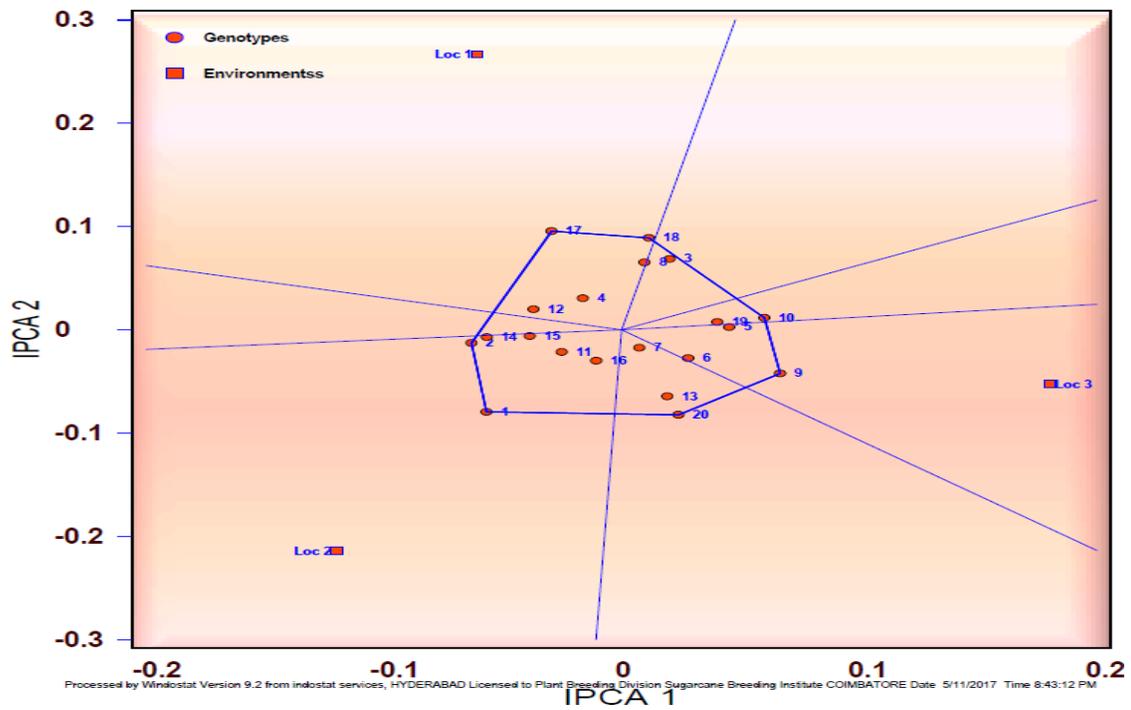


Fig.2 Intracation Biplot (AMMI 2) for grain yield plant⁻¹(g)

In interaction principle axis of AMMI biplot, first interaction principle axis (IPCA I) are favorable for all characters but second interaction principle axis (IPCA II) are favorable for characters such as spikelets fertility, grain yield plot⁻¹ (kg), number of panicles square meter⁻¹, protein content (%), iron content (ppm), amylose content (%), grain yield plant⁻¹(g) and total number of spikelets panicle⁻¹.

Genotypes viz., RTN-1201-51-2-1-5-48, RTN-1211-5-1-3-5 and RTN-1201-5-1-3-14 were stable for Shirgaon and Dapoli environments for the traits viz., grain yield plant⁻¹, grain yield plot⁻¹, protein content (%), zinc content (ppm), iron content (ppm), amylose content (%), genotypes viz., RTN-1201-51-2-1-5-48 and RTN-1211-6-1-3-1-8 were stable for Shirgaon environment only, while as genotype RTN-1201-13-2-2-1-32 was stable for for all yield contributing characters across the three environments.

Genotype, RTN-1201-13-2-2-1-32 is most favourable for all the characters in the entire three environments, with high yield, maximum plant height, and more content of micronutrients and Genotype, RTN-1211-4-2-1-1 is stable for grain yield plot⁻¹, grain yield plant⁻¹ and protein content could be commercially exploited after testing in state multilocation and national trials or may be utilized for further studies.

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How to cite this article:

Waghmode. B. D., M. R. Chavan, N. G. Sonone and Bhave. S. G. 2020. AMMI Biplot analysis for Stability of Grain Yield and Yield Contributing Traits in Promising Bio-Fortified Red Kernel Genotypes of Rice (*Oryza sativa* L.). *Int.J.Curr.Microbiol.App.Sci.* 9(03): 1820-1832. doi: <https://doi.org/10.20546/ijcmas.2020.903.211>